In the Claims

1-57. (Previously canceled)

58. (Currently amended) A method of identifying a non-oligomeric organic compound ~~less than 2000 daltons in size,~~ that has the greatest relative affinity for a target protein comprising:

(a) contacting in a mixture a target protein with a library of non-oligomeric organic compounds, less than 2000 daltons in size, that are each capable of binding covalently to a chemically reactive group on the target protein, thereby forming a target protein-compound conjugate;

(b) analyzing the mixture by mass spectrometry; and

(c) detecting the most abundant target protein-compound conjugate that is formed, and

(d) determining the identity of the non-oligomeric organic compound present in said target protein-compound conjugate as the non-oligomeric organic compound having the greatest relative affinity for the target protein,

wherein said non-oligomeric organic compound is a novel ligand for said target protein.

59. (Currently amended) The method of claim 58 wherein the novel ligand is less than 1500 daltons in size.

60. (Previously canceled)

61. (Currently amended) The method of claim 58 wherein the novel ligand is less than 750 daltons in size.

62. (Previously presented) The method of claim 58 wherein said target protein is a protease.

63. (Previously presented) The method of claim 58 wherein said target protein is a kinase.

64. (Previously presented) The method of claim 58 wherein said target protein is a dephosphorylase (phosphatase).

65. (Previously presented) The method of claim 58 wherein said target protein is a TNF receptor.

66. (Previously presented) The method of claim 58 wherein said target protein is mdm2 receptor.

67.-80. (Previously canceled)

81. (Previously presented) The method of claim 58 wherein said chemically reactive group is an -SH group, a protected -SH group or an activated -SH group.

82. (Currently amended) The method of claim 81 wherein said -SH group, protected -SH group or activated -SH group is ~~associated with~~ part of a cysteine residue of said target protein.

83. (Previously presented) The method of claim 58 wherein the library comprises at least two members.

84. (Previously presented) The method of claim 58 wherein the library comprises at least 25 members.

85. (Previously presented) The method of claim 58 wherein the library comprise at lest 100 members.

86. (Currently amended) A competition assay comprising:

(a) contacting in a mixture a target protein, a reducing agent, and at least two compounds that are less than 2000 daltons and capable of forming a disulfide bond with the target protein thereby forming a target protein-compound conjugate;

(b) analyzing the mixture by mass spectrometry; and

(c) detecting the most abundant ~~target protein-compound~~ target protein-compound conjugate that is formed.

87. (Currently amended) The assay of claim ~~96~~ 86 further comprising determining the identify of the compound that is disulfide bonded to the target protein in the most abundant target protein-compound conjugate that is formed.

88. (New) The assay of claim 86 wherein the compounds are less than 1500 daltons in size.

89. (New) The assay of claim 86 wherein the compounds are less than 750 daltons in size.

90. (New) The assay of claim 86 wherein said target protein in a protease.

91. (New) The assay of claim 86 wherein said target protein is a kinase.

92. (New) The assay of claim 86 wherein said target protein is a dephosphorylase (phosphatase).

93. (New) The assay of claim 86 wherein said target protein is a TNF receptor.

94. (New) The assay of claim 86 wherein said target protein is an mdm2 receptor.

95. (New) The assay of claim 86 wherein said mixture is contacted with at least 25 compounds.

96. (New) The assay of claim 86 wherein said mixture is contacted with at least 100 compounds.